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Leukocytes identification using augmentation and transfer learning based convolution neural network

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ABSTRACT

Most haematological diseases can be diagnosed using the morphological analysis of the microscopic blood image. The basic routine of the morphological analysis can be performed using the microscopic device which requires the skills and experiences of the haematologists. An inexperienced haematologist can lead to critical human errors. Therefore, this paper aims to propose an automated classification system used to classify different types of leukocytes based on the convolution neural network (CNN) algorithm. CNN has achieved robust performance in various fields especially in medical applications. A dataset of microscopic blood cells images of the conforming tags (basophil, eosinophil, erythroblast, lymphocyte, monocyte, neutrophil, and platelet) was used to train and test the proposed algorithm. The augmentation and deep transfer approaches were used to improve and enhance the performance of the CNN algorithm. The overall accuracy of the proposed classifier was 98% with Visual Geometry Group-19 (VGG-19). The obtained accuracy was higher than the state-of-art algorithms. To conclude that using the augmentation and deep transfer approaches with VGG-19 can obtain better classification results.

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1. INTRODUCTION

The blood is the liquid that flow inside the human body through the vessel. It consists of three main parts known as cells, these cells are: red blood cells (RBCs), white blood cells (WBCs), and platelets [1]. The human immune system mainly depended on leukocytes (white blood cells) which in turn are strictly connected to several diseases [2]. Leukocytes are mostly separated into five sorts (neutrophils, basophils, eosinophils, monocytes, and lymphocytes) [3]. Diagnosis the sort of Leukocytes has a serious necessity on the physician's medical knowledge and their experience. The detection of each type of leukemia differs for physician to another in terms of the skill to discover WBCs, thus this issue can lead to critical errors [4]. Where, hematologists usually detect blood cells number and classify them using microscope device. This procedure is wasteful, and the count and cataloguing outcomes are affected by human errors [5], [6]. To solve these problems, recently studies focusing on using artificial intelligence (AI) to address these problems, either by the using support vector machine algorithm (SVM) based on machine learning, or the further progressive approaches are convolution neural network algorithm (CNN) [6]-[13].

Prinyakupt and Pluempitiwiriyawej, presented the WBCs classification based on the naive and linear Bayesian schemes [14]. The procedure was used 477 blood cell images using nuclear and cell segmentation. Furthermore, Gupta *et al.*, presented an enhanced binary batch algorithm to classify WBCs according to the

texture and shapes. It attained a regular output classification accuracy of 92.77% on 237 images [15]. Although, these schemes attained higher outcome, cell images need to be pre-segmented that consume time and produce human error as well as losing some important features during segmentation process.

To overcome the previous problems, the deep CNN show higher performance and excellent results in the field of medical application [16]-[18]. Zhang *et al.* presented a synergic deep learning (SDL) prototypical to answer several issues of intra-class and inter-class variances produced by medical tomography and pathological variety [19]. Ma *et al*. proposed blood cell image classification algorithm based on a deep convolutional generative adversarial network (DC-GAN) and residual neural network (ResNet). The proposed system deals with white blood cell (WBC) only, which make it a little complex, time consuming and excluded the red blood cell [1]. It is also shown relatively low output accuracy 91%.

In this study, the convolution neural network algorithm based on the deep transfer learning has been proposed. These frameworks can present the complex procedure of segmentation and extraction features likened with the old-style machine learning system. It offers the solution of the tricky into an end-to-end simple method, and solve the fault produced by the phases for example the segmentation and feature enhancement in the conventional algorithm, which can improve the acknowledgement and classification of blood cells.

2. METHOD

A collection of blood cells images of the conforming tags (basophil, eosinophil, erythroblast, lymphocyte, monocyte, neutrophil, and platelet) were used as a training and testing dataset. Online available of microscopic high-quality peripheral blood cell images dataset has been used in this study [20]. Before the training process of the CNN architecture, all images were considered for the being of related.

The predicted approach comprises a series of processing steps, instead of using long term enhancement methods to produce the suitable algorithm that boost the pre-trained network performance. Most of the previous studies used deep augmenting approach to generalize and eliminate over fitting in their model without figure out the important of using the objective of this process and make it a facility to compensate of complex image processing steps [21]-[25]. The proposed algorithm facilitated the augmentation method in smart procedure to reduce the image processing steps. The framework of the classification system is shown in Figure 1.

Figure 1. The framework of the proposed blood cells classification system

2.1. Convolution neural network (CNN)

CNN or ConvNet is a deep learning algorithm consisting of a number of layers. CNN has achieved an excellent performance in the various fields particularly in medical applications [26], [27]. The CNN has been reduced using sharing biases and weights comparing to other neural network approaches. The structure of the CNN composes of fives layers: input, convolution, pooling, connected hidden, and softmax layers. The input of the neural network is an input layer representing pixels matrix of the target image. Red green blue (RGB) image is considered as an input image in the most of the CNN architecture.

Convolution layers are the most important layer of CNN. The convolution procedure of the input image is performed at the convolution layers to extract the feature maps. The Kernel filter is the element that implements the convolution operation in this layer. The kernel is applied to the local receptive field of the target image. Dot product is performed between a patch of the image and the kernel as shown in (1) [28]. The W symbol in (1) refers to the filter weight. While the b is the filter bias and the x is the image patch.

$$\sum_i w_i \, x_i + \mathrm{b} \tag{1}$$

The sub-sampling layer or the pooling layer is used to minimise the input image size, therefore the training computations and parameters of CNN will be reduced. The max-pooling layer has been mostly used. The fully connected hidden layers follow the pooling and convolution layers. At these layers used to connect the neurons of the first connected layers. The image feature maps are combined to use in the

classification processing of the images. The number of classes in the input images is equal to the number of neurons in the last fully connected layer.

2.2. Augmentation approach

The refining classification accuracy also be contingent on the number, and orientation of the database images. Based on that the augmentation technique is used. The augmentation method involved random reflection, and random rotation in angles (0-360), as shown in Figure 2. The benefit of these steps is to improve the CNN vision for blood cell features. It also boosts the model generalization. As a result, it improves the performance of the designed network [29].

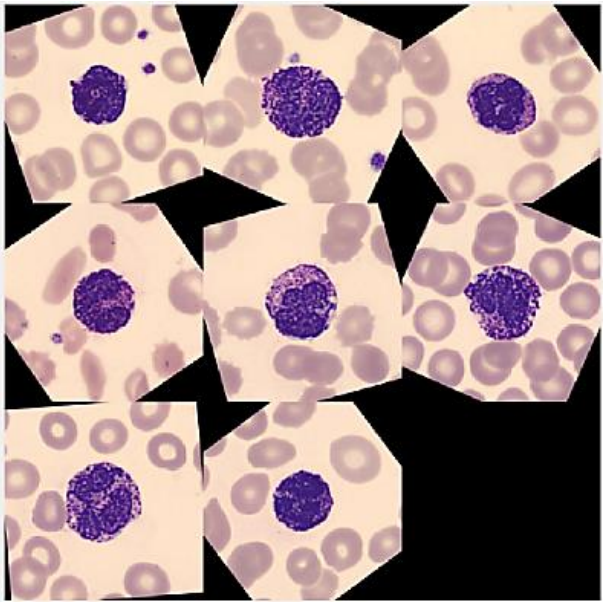


Figure 2. The generated blood cell images by transferred VGG-19

2.3. Deep transfer approach

The main goal of the deep transfer approach is to reuse the knowledge of the used model that had been already acquired good knowledge through training and testing with a wide range of the global net dataset. This acquired knowledge can use to solve the new task of a new specific database. This approach will allow reducing the required dataset for the training model, in addition to superior improvement for learning performance [16]. The performance of the transfer model for diagnosing blood cell limited by several issues. For example, the chosen pre-trained deep learning model, the kind and amount of training samples, and the pre-processing steps. This study depends on the weights of the transfer method that learns from shared weights among the source and target of pre-trained models. Therefore, it can be used to deliver more improvements in classification accuracy as well as reduce the total training interval [30]-[32].

2.4. Pre-trained model

The deep prognostic prototypical has been considered based on a pre-trained model, which was established by Oxford Visual Geometry Group [VGG] and call a VGG-19. The VGG pre-trained is constructed on 3×3 convolution layers. Then, the extra Conv and Relu layers are added to upsurge the depth of the model. Lastly, the max-pooling layer is used to condense the size of output features which are more willingly learned by a fully connected layer of 4,096 nodes [33].

In this paper, the fully connected layer has been settled to the number of classified sorts, which will improve the model performance and reduced the training time. Figure 3 shows the proposed model construction. Figure 4 shows the 64 channels of the features extracted at the first convolution layer.

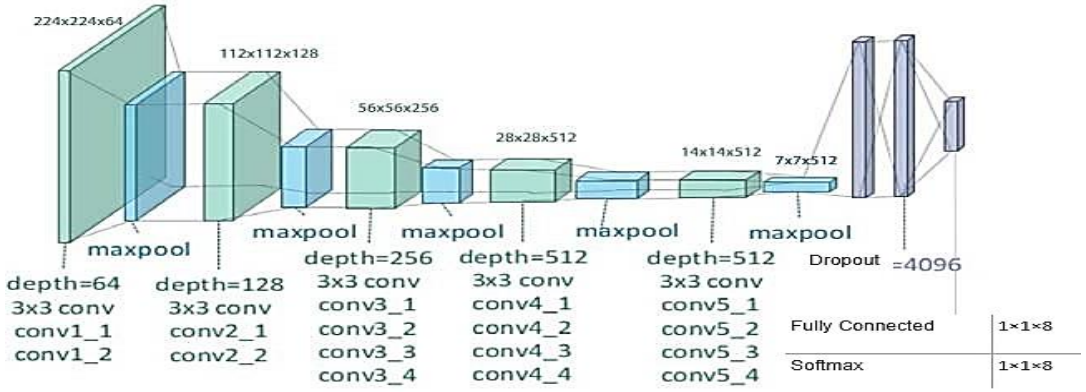


Figure 3. The proposed model of transferred pre-trained VGG-19

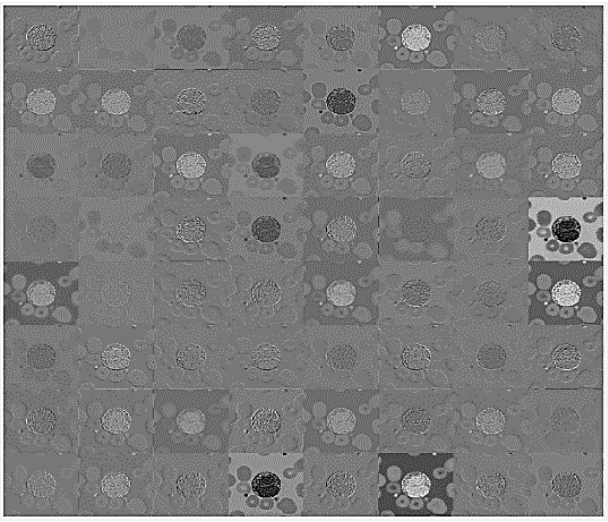


Figure 4. The feature channels of blood cell image from the first convolution layer of the proposed transferred VGG-19 model

3. RESULTS AND DISCUSSION

During training the proposed model, each type of blood cell image has been used. The augmentation process included such as reflex and rotation has also been used to produce training samples. After 10 epochs, the entire model produced upright results, the test loss touched the least value, and the agreeing test output validation accuracy was 98.15% with elapse time: 521 min, and maximum iteration: 6,800. The confusion matrix is shown in Figure 5. While Figure 6 represented the plotting of training progress of 10 epochs for the proposed transfer VGG.

The accuracy of both validation and training are shown in Figure 6(a). The training accuracy of the proposed model starts at 70% and increased with every epoch during training. The loss achieved at the end of each epoch is illustrated in Figure 6(b). The model shows a small rate of loss and a large rate of classification.

The output classification results show a superior comparison to state-of-art studies. This was obtained by choosing the correct pre-trained model VGG-19 that proved its ability to classify the different medical images in various areas [34]. It is also worth mentioning that a well understanding of the augmentation method and using the deep transfer leering approach can be lead to an increase in the accuracy of the classification system. All these approaches led to gain superior classification results compared to the previous studies as shown in Table 1.

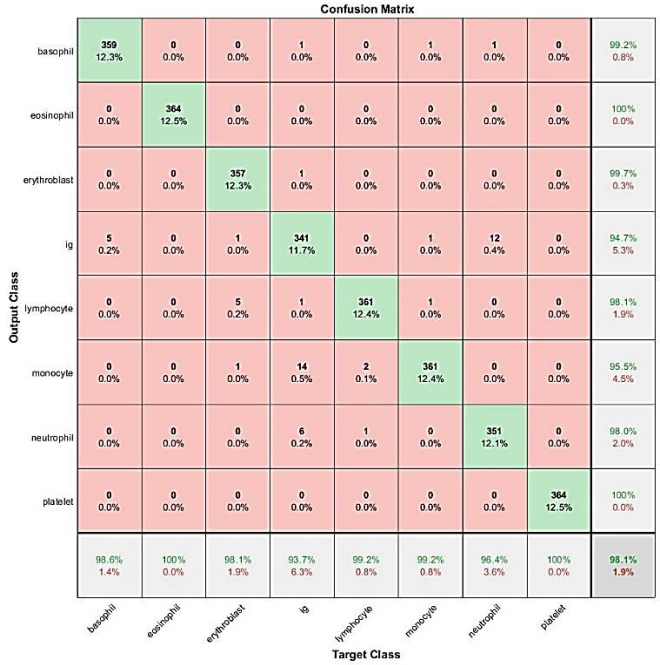
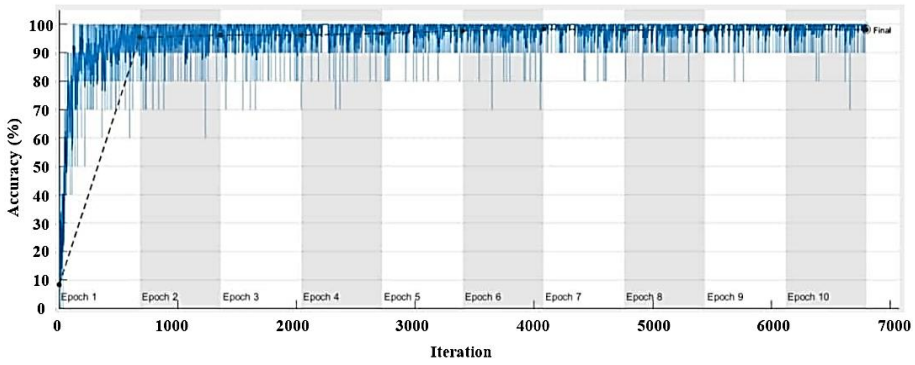
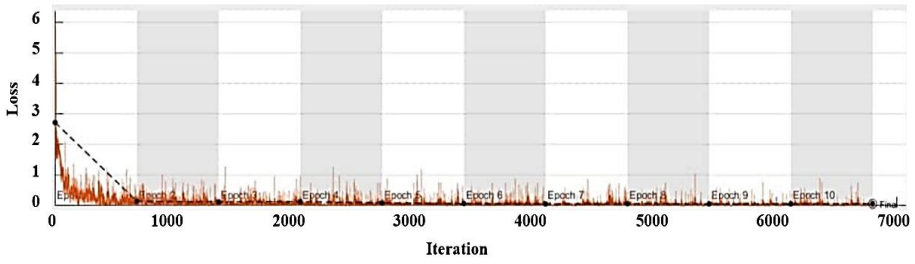


Figure 5. Performance of the artificial neural network from transferred VGG-19



(a)



(b)

Figure 6. Training progress plot of the transferred pre-trained VGG-19: (a) accuracy and (b) loss

Table 1. The comparison between the proposed and the state-of-arts systems

Model	Accuracy %
DC-GAN-ResNet [1]	91.68
VGG-16 [23]	96
Inceptionv3 [23]	95
Proposed model	98.1

4. CONCLUSION

Using the convolution neural network algorithm based on the augmentation method and deep transfer learning was the main contribution in this study. The augmentation method used to reduce the pre-processing time for features extraction, while, the deep transfer learning used to obtain a higher accuracy comparing with the previous studies. The results of this study also confirm that using of augmentation method not only reduces the pre-processing time but also evades the fault produced by the segmentation and feature enhancement stages in the conventional algorithm. The overall accuracy that has been obtained for the proposed classification system is 98% with VGG-19 which is satisfactory and higher than the previous studies. This study focused on the certain types of blood cells (leukocytes) which play an important role in the function of the human immune system. This is considered as the base for a new diagnosis system to help haematologists to give the right decision and reduce human error.

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